SEQUENCE LISTING

<110> Bryan, Bruce
     Szent-Gyorgyi, Christopher
     Szczepaniak, William

<120> RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT SCREENING AND NOVELTY ITEMS

<130> 24729-128

<140> Not Yet Assigned
<141> Herewith

<150> 60/189,691
<151> 2000-03-15

<150> 09/277,716
<151> 1999-03-26

<150> 08/757,046
<151> 1996-11-25

<150> 08/597,274
<151> 1996-02-06

<150> 08/908,909
<151> 1997-08-08

<150> 08/990,103
<151> 1997-12-12

<160> 33

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1196
<212> DNA
<213> Renilla reniformis

<220>
<221> CDS
<222> (1)...(942)
<223> Renilla reniformas luciferase

<400> 1
```
agc tta aag atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg        48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
 1               5                   10                  15

atg ata act ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt        96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
            20                  25                  30

ctt gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat       144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
            35                  40                  45

gct gtt att ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga       192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
        50                  55                  60
```

```
cat gtt gtg cca cat att gag cca gta gcg cgg tgt att ata cca gat        240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
 65              70              75              80

ctt att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg        288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
             85              90              95

tta ctt gat cat tac aaa tat ctt act gca tgg ttg aac ttc tta att       336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
            100             105             110

tac caa aga aga tca ttt ttt gtc ggc cat gat tgg ggt gct tgt ttg       384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
            115             120             125

gca ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt       432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
            130             135             140

cac gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct       480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145             150             155             160

gat att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa       528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
            165             170             175

atg gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa       576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
            180             185             190

atc atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca       624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
            195             200             205

ttc aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt       672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
            210             215             220

gaa atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt       720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225             230             235             240

agg aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg       768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
            245             250             255

ttt att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc       816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
            260             265             270

gcc aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat       864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
            275             280             285

ttt tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg       912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
            290             295             300

ttc gtt gag cga gtt ctc aaa aat gaa caa taattacttt ggttttttat         962
Phe Val Glu Arg Val Leu Lys Asn Glu Gln
305             310

ttacatttt cccgggttta ataatataaa tgtcatttc aacaatttta ttttaactga       1022
```

-2-

```
atatttcaca gggaacattc atatatgttg attaatttag ctcgaacttt actctgtcat    1082
atcattttgg aatattacct cttttcaatga aactttataa acagtggttc aattaattaa    1142
tatatattat aattacattt gttatgtaat aaactcggtt ttattataaa aaaa           1196
```

```
<210> 2
<211> 1822
<212> DNA
<213> Cypridina hilagendorfii luciferase

<220>
<221> CDS
<222> (1)...(1665)
<223> Cypridina hilgendorfii luciferase

<400> 2
atg aag cta ata att ctg tct att ata ttg gcc tac tgt gtc aca gtc     48
Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val
 1               5                  10                  15

aac tgc cag gat gca tgt cct gta gaa gct gaa gca ccg tca agt aca     96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
            20                  25                  30

cca aca gtc cca aca tct tgt gaa gct aaa gaa gga gaa tgt atc gat    144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
        35                  40                  45

acc aga tgc gca aca tgt aaa cga gac ata cta tca gac gga ctg tgt    192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
    50                  55                  60

gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gta att    240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
65                  70                  75                  80

gaa tcc aga gta gaa gct gct gga tat ttt aga acg ttt tac gcc aaa    288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
                85                  90                  95

aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct cga gga acc    336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
            100                 105                 110

aag ggt ggc gac tgg tct gta acc ctc acc atg gag aat cta gat gga    384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
        115                 120                 125

cag aag gga gct gta ctg act aag aca aca ctg gag gta gta gga gac    432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
    130                 135                 140

gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga    480
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145                 150                 155                 160

gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc    528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
                165                 170                 175

att gct gtt gtc gaa ata ccc ggc ttc aat att aca gtc atc gaa ttc    576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
                180                 185                 190
```

```
ttt aaa cta atc gtg ata gat att ctg gga gga aga tct gtg aga att        624
Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
        195             200             205

gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat        672
Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
210             215             220

ctg gag atg aat gac gct gat gac ttt act aca gac gca gat cag ctg        720
Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
225             230             235             240

gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tac        768
Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
                245             250             255

ggg aat cct tct gat atc gaa tac tgc aaa ggt ctc atg gag cca tac        816
Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
                260             265             270

aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act ctg tcc        864
Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
        275             280             285

tgc gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc        912
Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
        290             295             300

ctt ttc gac tat gtt gag aca tgc gct gca ccg gaa acg aga gga acg        960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
305             310             315             320

tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gcc aga      1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
                325             330             335

tat caa ttc cag ggc cca tgc aaa gag ctt ctg atg gcc gca gac tgt      1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Leu Leu Met Ala Ala Asp Cys
                340             345             350

tac tgg aac aca tgg gat gta aag gtt tca cat aga gat gtt gag tca      1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
                355             360             365

tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta      1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
370             375             380

gat ttg att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta      1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
385             390             395             400

tct atc ccg tac agt tct gag aac aca tcc ata tac tgg cag gat gga      1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
                405             410             415

gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc      1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
                420             425             430

aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga      1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly
                435             440             445

aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat      1392
```

```
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
    450                 455             460

ttc ttt gac gca gaa gga gca tgc gct ctg acc ccc aat ccc cca gga      1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
465             470             475                 480

tgt aca gag gag cag aaa cca gaa gct gag cga ctc tgc aat agt cta      1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu
                485             490             495

ttt gat agt tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac      1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
            500             505             510

cgt att gca cga tgt atg tac gag tat tgc ctg agg gga cag caa gga      1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
        515             520             525

ttc tgt gac cat gct tgg gag ttc aaa aaa gaa tgc tac ata aag cat      1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
    530             535             540

gga gac act cta gaa gta cca cct gaa tgc caa taaatgaaca aagatacaga    1685
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
545             550             555

agctaagact actacagcag aagataaaag agaagctgta gttcttcaaa aacagtatat    1745
tttgatgtac tcattgttta cttacataaa aataaattgt tattatcata acgtaaagaa    1805
aaaaaaaaaa aaaaaaa                                                   1822


<210> 3
<211> 1644
<212> DNA
<213> Luciola cruciata

<220>
<221> CDS
<222> (1)...(1644)
<223> Luciola cruciata luciferase

<400> 3
atg gaa aac atg gaa aac gat gaa aat att gta gtt gga cct aaa ccg       48
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys Pro
 1               5                   10                  15

ttt tac cct atc gaa gag gga tct gct gga aca caa tta cgc aaa tac       96
Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg Lys Tyr
             20                  25                  30

atg gag cga tat gca aaa ctt ggc gca att gct ttt aca aat gca gtt      144
Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Val
         35                  40                  45

act ggt gtt gat tat tct tac gcc gaa tac ttg gag aaa tca tgt tgt      192
Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
     50                  55                  60

cta gga aaa gct ttg caa aat tat ggt ttg gtt gtt gat ggc aga att      240
Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
 65                  70                  75                  80

gcg tta tgc agt gaa aac tgt gaa gaa ttt ttt att cct gta ata gcc      288
Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Ile Ala
```

-5-

```
                 85                        90                        95

 gga ctg ttt ata ggt gta ggt gtt gca ccc act aat gag att tac act    336
Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
            100                 105                 110

tta cgt gaa ctg gtt cac agt tta ggt atc tct aaa cca aca att gta    384
Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
            115                 120                 125

ttt agt tct aaa aaa ggc tta gat aaa gtt ata aca gta cag aaa aca    432
Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
    130                 135                 140

gta act act att aaa acc att gtt ata cta gat agc aaa gtt gat tat    480
Val Thr Thr Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
145                 150                 155                 160

cga gga tat caa tgt ctg gac acc ttt ata aaa aga aac act cca cca    528
Arg Gly Tyr Gln Cys Leu Asp Thr Phe Ile Lys Arg Asn Thr Pro Pro
                165                 170                 175

ggt ttt caa gca tcc agt ttc aaa act gtg gaa gtt gac cgt aaa gaa    576
Gly Phe Gln Ala Ser Ser Phe Lys Thr Val Glu Val Asp Arg Lys Glu
            180                 185                 190

caa gtt gct ctt ata atg aac tct tcg ggt tct acc ggt ttg cca aaa    624
Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
            195                 200                 205

ggc gta caa ctt act cac gaa aat aca gtc act aga ttt tct cat gct    672
Gly Val Gln Leu Thr His Glu Asn Thr Val Thr Arg Phe Ser His Ala
    210                 215                 220

aga gat ccg att tat ggt aac caa gtt tca cca ggc acc gct gtt tta    720
Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Val Leu
225                 230                 235                 240

act gtc gtt cca ttc cat cat ggt ttt ggt atg ttc act act cta ggg    768
Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
                245                 250                 255

tat tta att tgt ggt ttt cgt gtt gta atg tta aca aaa ttc gat gaa    816
Tyr Leu Ile Cys Gly Phe Arg Val Val Met Leu Thr Lys Phe Asp Glu
                260                 265                 270

gaa aca ttt tta aaa act cta caa gat tat aaa tgt aca agt gtt att    864
Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Thr Ser Val Ile
            275                 280                 285

ctt gta ccg acc ttg ttt gca att ctc aac aaa agt gaa tta ctc aat    912
Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Lys Ser Glu Leu Leu Asn
            290                 295                 300

aaa tac gat ttg tca aat tta gtt gag att gca tct ggc gga gca cct    960
Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
305                 310                 315                 320

tta tca aaa gaa gtt ggt gaa gct gtt gct aga cgc ttt aat ctt ccc    1008
Leu Ser Lys Glu Val Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
                325                 330                 335

ggt gtt cgt caa ggt tat ggt tta aca gaa aca aca tct gcc att att    1056
Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
            340                 345                 350
```

-6-

```
att aca cca gaa gga gac gat aaa cca gga gct tct gga aaa gtc gtg      1104
Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
        355                 360             365

ccg ttg ttt aaa gca aaa gtt att gat ctt gat acc aaa aaa tct tta      1152
Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Ser Leu
    370                 375             380

ggt cct aac aga cgt gga gaa gtt tgt gtt aaa gga cct atg ctt atg      1200
Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
385             390             395                 400

aaa ggt tat gta aat aat cca gaa gca aca aaa gaa ctt att gac gaa      1248
Lys Gly Tyr Val Asn Asn Pro Glu Ala Thr Lys Glu Leu Ile Asp Glu
            405             410                 415

gaa ggt tgg ctg cac acc gga gat att gga tat tat gat gaa gaa aaa      1296
Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
        420             425                 430

cat ttc ttt att gtc gat cgt ttg aag tct tta atc aaa tac aaa gga      1344
His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
        435             440             445

tac caa gta cca cct gcc gaa tta gaa tcc gtt ctt ttg caa cat cca      1392
Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
    450             455             460

tct atc ttt gat gct ggt gtt gcc ggc gtt cct gat cct gta gct ggc      1440
Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly
465             470             475                 480

gag ctt cca gga gcc gtt gtt gta ctg gaa agc gga aaa aat atg acc      1488
Glu Leu Pro Gly Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr
            485             490                 495

gaa aaa gaa gta atg gat tat gtt gca agt caa gtt tca aat gca aaa      1536
Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
            500             505             510

cgt tta cgt ggt ggt gtt cgt ttt gtg gat gaa gta cct aaa ggt ctt      1584
Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
            515             520             525

act gga aaa att gac ggc aga gca att aga gaa atc ctt aag aaa cca      1632
Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro
        530             535             540

gtt gct aag atg                                                      1644
Val Ala Lys Met
545
```

```
<210> 4
<211> 1820
<212> DNA
<213> Vargula (cypridina)

<220>
<221> CDS
<222> (1)...(1665)
<223> Vargula (cypridina) luciferase

<400> 4
```

-7-

```
atg aag ata ata att ctg tct gtt ata ttg gcc tac tgt gtc acc gac        48
Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp
 1               5                  10                  15

aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca        96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
                20              25                  30

cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat       144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
            35                  40                  45

acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt       192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
        50                  55                  60

gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att       240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
65                  70                  75                  80

gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa       288
Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys
                85                  90                  95

aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc       336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
                100                 105                 110

aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga       384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
            115                 120                 125

cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac       432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp
        130                 135                 140

gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga       480
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145                 150                 155                 160

gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc       528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
                165                 170                 175

att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc       576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
                180                 185                 190

ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtc aga att       624
Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
            195                 200                 205

gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat       672
Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
        210                 215                 220

ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg       720
Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
225                 230                 235                 240

gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat       768
Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
                245                 250                 255

ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac       816
```

-8-

```
Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
            260                 265                 270

aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act cta tcc    864
Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
        275                 280                 285

tgt gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc    912
Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
        290                 295                 300

ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg    960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
305                 310                 315                 320

tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga   1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
                325                 330                 335

tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt   1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys
                340                 345                 350

tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca   1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
                355                 360                 365

tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta   1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
            370                 375                 380

gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta   1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
385                 390                 395                 400

tct atc ccg tac agc tct gag aac act tcc ata tac tgg cag gat gga   1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
                405                 410                 415

gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc   1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
                420                 425                 430

aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gca   1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Ala
                435                 440                 445

aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat   1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
            450                 455                 460

ttc ttt gac gca gaa gga gca tgc gct cta acc ccc aac ccc cca gga   1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
465                 470                 475                 480

tgt aca gag gaa cag aaa cca gaa gct gag cga ctt tgc aat aat ctc   1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu
                485                 490                 495

ttt gat tct tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac   1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
                500                 505                 510

cgg att gcc cga tgt atg tac gag tat tgc ctg agg gga caa caa gga   1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
```

-9-

```
              515                    520                    525
ttt tgt gac cat gct tgg gag ttc aag aaa gaa tgc tac ata aaa cat      1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
    530                    535                    540

gga gac act cta gaa gta cca cct gaa tgt caa taaacgtaca aagatacaga    1685
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
545                    550                    555

agctaaggct actacagcag aagataaaaa agaaactgta gttccttcaa aaaccgtgta    1745
ttttatgtac tcattgttta attagagcaa aataaattgt tattatcata acttaaacta    1805
aaaaaaaaaa aaaaa                                                      1820


<210> 5
<211> 958
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (115)...(702)
<223> Apoequorin-encoding gene

<400> 5
gggggggggg gggggggggg gggggggggg gggaatgcaa ttcatctttg catcaaagaa       60
ttacatcaaa tctctagttg atcaactaaa ttgtctcgac aacaacaagc aaac atg        117
                                                             Met
                                                             1

aca agc aaa caa tac tca gtc aag ctt aca tca gac ttc gac aac cca      165
Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
            5                   10                  15

aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc aac      213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
            20                  25                  30

cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct gat      261
His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
        35                  40                  45

att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga cac      309
Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
50                  55                  60                  65

aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat ggt      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
                70                  75                  80

gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg gct      405
Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
                85                  90                  95

act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc cgt      453
Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg
            100                 105                 110

ata tgg ggt gat gct ttg ttt gat atc gtt gac aaa gat caa aat gga      501
Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly
        115                 120                 125

gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt atc      549
Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile
130                 135                 140                 145
```

-10-

```
atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat att      597
Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile
                150                 155                 160

gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat tta      645
Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
                165                 170                 175

gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt gga     693
Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly
                180                 185                 190

gct gtc ccc taagaagctc tacggtggtg atgcacccta ggaagatgat           742
Ala Val Pro
        195

gtgattttga ataaaacact gatgaattca atcaaaattt tccaatttt tgaacgattt    802
caatcgtttg tgttgatttt tgtaattagg aacagattaa atcgaatgat tagttgtttt    862
tttaatcaac agaacttaca aatcgaaaaa gtaaaaaaa aaaaaaaaa aaaaaaaaa       922
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                              958


<210> 6
<211> 591
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Recombinant Aequorin AEQ1

<400> 6
atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
  1               5                  10                  15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
                20                  25                  30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
                35                  40                  45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
        50                  55                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
 65                  70                  75                  80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
                100                 105                 110

cgt tta tgg ggt gat gca ttg ttc gat atc att gac aaa gac caa aat     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn
                115                 120                 125
```

```
gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gat ggc    432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly
    130             135             140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat    480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145             150             155                 160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat    528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165             170             175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt    576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180             185             190

gga gct gtc ccc taa                                                591
Gly Ala Val Pro
        195


<210> 7
<211> 591
<212> DNA
<213> Aequoria victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Recombinant Aequorin AEQ2

<400> 7
atg acc agc gaa caa tac tca gtc aag ctt aca tca gac ttc gac aac     48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
1               5                   10                  15

cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc     96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
                20                  25                  30

aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct    144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
            35                  40                  45

gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga    192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat    240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
65              70                  75                  80

ggt gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg    288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
                85                  90                  95

gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc    336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
            100             105             110

cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat    384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
            115             120             125
```

```
gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt    432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
    130             135             140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat    480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145             150             155             160

att gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat    528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165             170             175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt    576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
                180             185             190

gga gct gtc ccc taa                                                591
Gly Ala Val Pro
            195
```

```
<210> 8
<211> 591
<212> DNA
<213> Aequoria victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Recombinant Aequorin AEQ3

<400> 8
atg acc agc gaa caa tac tca gtc aag ctt aca tca gac ttc gac aac     48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
1               5               10              15

cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc     96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20              25              30

aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct    144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
            35              40              45

gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga    192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50              55              60

cac aaa gat gct gta gga gac ttc ttc gga gga gct gga atg aaa tat    240
His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr
65              70              75              80

ggt gtg gaa act gat tgg cct gca tac att gaa gga tgg aaa aaa ttg    288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
                85              90              95

gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc    336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
                100             105             110

cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat    384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
                115             120             125

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt    432
```

-13-

```
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
    130                 135             140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat      480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145             150                 155                 160

att gat gaa aat gga caa ctc gat gtt gat gag atg aca aga caa cat      528
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt      576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
                180                 185                 190

gga gct gtc ccc taa                                                   591
Gly Ala Val Pro
        195


<210> 9
<211> 567
<212> DNA
<213> Aequoria victoria

<220>
<221> CDS
<222> (1)...(567)
<223> Aequorin photoprotein

<400> 9
gtc aag ctt aca cca gac ttc gac aac cca aaa tgg att gga cga cac       48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1               5                   10                  15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct       96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
                20                  25                  30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt      144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
            35                  40                  45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc      192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
        50                  55                  60

ttc ttc gga gga gct gca atg aaa tat ggt gta gaa act gaa tgg cct      240
Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
 65                  70                  75                  80

gaa tac atc gaa gga tgg aaa aga ctg gct tcc gag gaa ttg aaa agg      288
Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg
                85                  90                  95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg      336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
                100                 105                 110

ttc gat atc att gac aaa gac caa aat gga gct att tca ctg gat gaa      384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu
                115                 120                 125

tgg aaa gca tac acc aaa tct gct ggc atc atc caa tcg tca gaa gat      432
Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp
    130                 135                 140
```

-14-

```
tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc     480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
145                 150                 155                 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg     528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
                165                 170                 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc               -567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
                180                 185
```

<210> 10
<211> 588
<212> DNA
<213> Aequoria victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Aequorin mutant w/increased bioluminescence
      activity

<400> 10
```
atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
  1                 5                  10                  15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
                20                  25                  30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
                35                  40                  45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
     50                  55                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
 65                  70                  75                  80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
                100                 105                 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
                115                 120                 125

gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc     432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
                130                 135                 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160
```

-15-

```
att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat      528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt      576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
                180                 185                 190

gga gct gtc ccc                                                       588
Gly Ala Val Pro
        195
```

<210> 11
<211> 588
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Recombinant site-directed Aequorin mutant

```
<400> 11
atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac       48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc       96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
                20                  25                  30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc      144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
            35                  40                  45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt      192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
        50                  55                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat      240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
65                  70                  75                  80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg      288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att      336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
                100                 105                 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat      384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
            115                 120                 125

gga gct att tca ctg gat tca tgg aaa gca tac acc aaa tct gct ggc      432
Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly
        130                 135                 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat      480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160
```

```
att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat    528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
            165             170             175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt    576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180             185             190

gga gct gtc ccc                                                    588
Gly Ala Val Pro
        195
```

<210> 12
<211> 588
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (1)...(588)
<223> Aequorin mutant with increased biolumenescence
      activity

<400> 12

```
atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac     48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc     96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc    144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
            35                  40                  45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt    192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
        50                  55                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat    240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
65                  70                  75                  80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg    288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att    336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
            100                 105                 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat    384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
            115                 120                 125

gca gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc    432
Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
        130                 135                 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat    480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160
```

```
att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat      528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165               170               175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt      576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
                180               185               190

gga gct gtc ccc                                                       588
Gly Ala Val Pro
            195
```

```
<210> 13
<211> 567
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (1)...(567)
<223> Recombinant apoaequorin (AQUALITEp)

<400> 13
gtc aag ctt aca cca gac ttc gac aac cca aaa tgg att gga cga cac       48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1               5                  10                  15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct       96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
                20                  25                  30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt      144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
                35                  40                  45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc      192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
        50                  55                  60

ttc ttc gga gga gct gga atg aaa tat ggt gta gaa act gaa tgg cct      240
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
 65                  70                  75                  80

gaa tac atc gaa gga tgg aaa aaa ctg gct tcc gag gaa ttg aaa agg      288
Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg
                    85                  90                  95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg      336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
                100                 105                 110

ttc gat atc att gac aaa gac caa aat gga gct att ctg tca gat gaa      384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu
                115                 120                 125

tgg aaa gca tac acc aaa tct gat ggc atc atc caa tcg tca gaa gat      432
Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp
                130                 135                 140

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc      480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
145                 150                 155                 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg      528
```

-18-

```
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
                165                 170                 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc                      567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
            180                 185
```

<210> 14
<211> 236
<212> PRT
<213> Vibrio fisheri

<400> 14

```
Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn
 1               5                   10                  15
Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
            20                  25                  30
Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
        35                  40                  45
Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
    50                  55                  60
Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
65                  70                  75                  80
Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
                85                  90                  95
His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
            100                 105                 110
Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
        115                 120                 125
Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
    130                 135                 140
Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
145                 150                 155                 160
Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
                165                 170                 175
Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp
            180                 185                 190
Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
        195                 200                 205
Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
    210                 215                 220
Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
225                 230                 235
```

<210> 15
<211> 1079
<212> DNA
<213> Renilla mulleri

<220>
<221> CDS
<222> (259)...(975)
<223> Renilla mulleri GFP

<400> 15

```
ggttatacac aagtgtatcg cgtatctgca gacgcatcta gtgggattat tcgagcggta     60
gtatttacgt cagacctgtc taatcgaaac cacaacaaac tcttaaaata agccacattt    120
acataatatc taagagacgc ctcatttaag agtagtaaaa atataatata tgatagagta    180
tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttgttaa tgcaatcgaa    240
agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta    291
                    Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
                     1               5                   10
```

-19-

```
caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac      339
Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
            15                  20                  25

cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc      387
His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
            30                  35                  40

aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt      435
Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
        45                  50                  55

gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc      483
Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe
60                  65                  70                  75

acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca      531
Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
                80                  85                  90

gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt      579
Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
                95                  100                 105

gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac      627
Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
            110                 115                 120

aga gtg gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg      675
Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met
    125                 130                 135

cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg      723
Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
140                 145                 150                 155

aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac      771
Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
                160                 165                 170

tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa      819
Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
            175                 180                 185

ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg      867
Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
            190                 195                 200

gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act      915
Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
    205                 210                 215

gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac      963
Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
220                 225                 230                 235

gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca        1015
Glu Trp Val  *


aataataatt ttttaaacaa ttatcaatgt tttgtgatat gtttgtaaaa aaaaaaaaaa    1075
aaaa                                                                 1079
```

<210> 16
<211> 238

```
<212> PRT
<213> Renilla mulleri

<400> 16
Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
 1               5                  10                  15
Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
            20                  25                  30
Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
        35                  40                  45
Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
    50                  55                  60
Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
65                  70                  75                  80
Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
                85                  90                  95
Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
            100                 105                 110
Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
            115                 120                 125
Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
    130                 135                 140
Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
145                 150                 155                 160
Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
                165                 170                 175
Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
            180                 185                 190
Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
        195                 200                 205
Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
    210                 215                 220
Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225                 230                 235

<210> 17
<211> 1217
<212> DNA
<213> Renilla  mulleri

<220>
<221> CDS
<222> (31)...(963)
<223> Renilla mulleri luciferase

<400> 17
cggcacgagg tttaagaatc aataaaaaaa atg acg tca aaa gtt tac gat cct      54
                                 Met Thr Ser Lys Val Tyr Asp Pro
                                  1               5


gaa tta aga aaa cgc atg att act ggt cca caa tgg tgg gca aga tgt     102
Glu Leu Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys
    10                  15                  20

aaa caa atg aat gtt ctt gat tca ttt att aat tat tat gat tca gaa    150
Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu
25                  30                  35                  40

aaa cat gca gaa aat gca gtt ata ttt tta cat ggt aat gca gca tct   198
Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser
                45                  50                  55

tct tat tta tgg cgt cat gtt gta cca cat gtt gaa cca gtg gcg cga   246
Ser Tyr Leu Trp Arg His Val Val Pro His Val Glu Pro Val Ala Arg
            60                  65                  70
```

```
tgt att ata cca gat ctt ata ggt atg ggt aaa tca ggc aag tct ggt      294
Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly
        75              80                  85

aat ggt tcc tat aga tta cta gat cat tac aaa tat ctt act gaa tgg      342
Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Glu Trp
        90              95                  100

ttc aaa cat ctt aat tta cca aag aag atc att ttt gtc ggt cat gat      390
Phe Lys His Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp
105             110             115                 120

tgg ggt gct tgt tta gca ttt cat tat tgc tat gaa cat cag gat cgc      438
Trp Gly Ala Cys Leu Ala Phe His Tyr Cys Tyr Glu His Gln Asp Arg
                125             130             135

atc aaa gca gtt gtt cat gct gaa agt gta gta gat gtg att gaa tcg      486
Ile Lys Ala Val Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser
            140             145             150

tgg gac gaa tgg cct gat att gaa gaa gat att gct ttg att aaa tct      534
Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser
            155             160             165

gaa gaa gga gaa aaa atg gtt tta gag aat aac ttc ttc gtg gaa acc      582
Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr
        170             175             180

atg ttg cca tca aaa atc atg aga aag ttg gaa cca gag gaa ttt gct      630
Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala
185             190             195                 200

gct tat ctt gaa cca ttt aaa gag aaa ggt gaa gtt cgt cgt cca aca      678
Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr
                205             210             215

tta tca tgg cct cgt gaa atc cct ttg gta aaa ggt ggt aaa ccg gat      726
Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp
                220             225             230

gta gta gaa att gtc agg aat tat aat gct tat ctt cgt gca agt cat      774
Val Val Glu Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser His
            235             240             245

gat tta cca aaa atg ttt att gaa tct gat cca gga ttc ttt tcc aat      822
Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn
            250             255             260

gct att gtt gaa ggt gct aag aaa ttc cct aat act gaa ttt gtt aaa      870
Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys
265             270             275                 280

gtc aaa ggt ctt cat ttt tca caa gaa gat gca cct gat gaa atg gga      918
Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly
                285             290             295

aat tat ata aaa tcg ttt gtt gag cgt gtt ctt aaa aat gaa caa          963
Asn Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln
                300             305             310
```

```
taaactacca ggtttccatg ttgccacttt agctgggttt aataaatttc actatcaatt   1023
tgaacaattt cacattaatt ttaactatta aaaaattatg gacacaggga ttatatcaga   1083
tgattaattt agttgggaac aatgaatacc gaatattatg aattctcttt agctatttat   1143
aataatcaca ttcttatgta ataaaacttt gttttaataa attaatgatt cagaaaaaaa   1203
```

aaaaaaaaaa aaaa   1217

<210> 18
<211> 311
<212> PRT
<213> Renilla   mulleri

<400> 18
Met Thr Ser Lys Val Tyr Asp Pro Glu Leu Arg Lys Arg Met Ile Thr
 1   5   10   15
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
            20   25   30
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
        35   40   45
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
    50   55   60
Pro His Val Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
65   70   75   80
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                85   90   95
His Tyr Lys Tyr Leu Thr Glu Trp Phe Lys His Leu Asn Leu Pro Lys
            100   105   110
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
            115   120   125
Tyr Cys Tyr Glu His Gln Asp Arg Ile Lys Ala Val Val His Ala Glu
    130   135   140
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145   150   155   160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165   170   175
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180   185   190
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
            195   200   205
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
            210   215   220
Leu Val Lys Gly Gly Lys Pro Asp Val Val Glu Ile Val Arg Asn Tyr
225   230   235   240
Asn Ala Tyr Leu Arg Ala Ser His Asp Leu Pro Lys Met Phe Ile Glu
                245   250   255
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
                260   265   270
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
            275   280   285
Glu Asp Ala Pro Asp Glu Met Gly Asn Tyr Ile Lys Ser Phe Val Glu
    290   295   300
Arg Val Leu Lys Asn Glu Gln
305   310

<210> 19
<211> 765
<212> DNA
<213> Gaussia

<220>
<221> CDS
<222> (37)...(594)

<400> 19
gcacgagggt actcaaagta tcttctggca gggaaa atg gga gtg aaa gtt ctt   54
                                        Met Gly Val Lys Val Leu
                                         1   5

ttt gcc ctt att tgt att gct gtg gcc gag gcc aaa cca act gaa aac   102
Phe Ala Leu Ile Cys Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn

                                -23-

```
                    10                    15                    20
aat gaa gat ttc aac att gta gct gta gct agc aac ttt gct aca acg    150
Asn Glu Asp Phe Asn Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr
         25                    30                    35

gat ctc gat gct gac cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt    198
Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu
     40                    45                    50

gag gta ctc aaa gaa atg gaa gcc aat gct agg aaa gct ggc tgc act    246
Glu Val Leu Lys Glu Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr
 55                    60                    65                    70

agg gga tgt ctg ata tgc ctg tca cac atc aag tgt aca ccc aaa atg    294
Arg Gly Cys Leu Ile Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met
                 75                    80                    85

aag aag ttt atc cca gga aga tgc cac acc tat gaa gga gac aaa gaa    342
Lys Lys Phe Ile Pro Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu
                 90                    95                   100

agt gca cag gga gga ata gga gag gct att gtt gac att cct gaa att    390
Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile
             105                   110                   115

cct ggg ttt aag gat ttg gaa ccc atg gaa caa ttc att gca caa gtt    438
Pro Gly Phe Lys Asp Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val
         120                   125                   130

gac cta tgt gta gac tgc aca act gga tgc ctc aaa ggt ctt gcc aat    486
Asp Leu Cys Val Asp Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn
135                   140                   145                   150

gtg caa tgt tct gat tta ctc aag aaa tgg ctg cca caa aga tgt gca    534
Val Gln Cys Ser Asp Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala
                 155                   160                   165

act ttt gct agc aaa att caa ggc caa gtg gac aaa ata aag ggt gcc    582
Thr Phe Ala Ser Lys Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala
                 170                   175                   180

ggt ggt gat taa tcctaataga atactgcata actggatgat gatatactag        634
Gly Gly Asp  *
             185

cttattgctc ataaaatggc catttttgt aacaaatcga gtctatgtaa ttcaaaatac   694
ctaattaatt gttaatacat atgtaattcc tataaatata atttatgcaa tccaaaaaaa   754
aaaaaaaaaa a                                                        765

<210> 20
<211> 185
<212> PRT
<213> Renilla mulleri

<400> 20
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
 1               5                   10                   15
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
         20                    25                    30
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
             35                    40                    45
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
         50                    55                    60
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
```

```
65                        70                        75                        80
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                        85                        90                        95
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
                100                       105                       110
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
            115                       120                       125
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
        130                       135                       140
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                       150                       155                       160
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                    165                       170                       175
Asp Lys Ile Lys Gly Ala Gly Gly Asp
                180                       185
```

<210> 21
<211> 1146
<212> DNA
<213> Gaussia

<220>
<221> CDS
<222> (1)...(1146)
<223> Nucleotide sequence encoding a CBD-Gaussia
      luciferase fusion protein

<400> 21

```
atg tca gtt gaa ttt tac aac tct aac aaa tca gca caa aca aac tca      48
Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
 1               5                  10                      15

att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat      96
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
                20                  25                  30

tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa     144
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
            35                  40                  45

gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc     192
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
        50                  55                  60

tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca     240
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
 65                  70                  75                      80

gca agc cca aca tca acc tat gat aca tat gtt gaa ttt gga ttt gca     288
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
                85                  90                      95

agc gga gca gct act ctt aaa aaa gga caa ttt ata act att caa gga     336
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
            100                 105                 110

aga ata aca aaa tca gac tgg tca aac tac act caa aca aat gac tat     384
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
            115                 120                 125

tca ttt gat gca agt agt tca aca cca gtt gta aat cca aaa gtt aca     432
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
            130                 135                 140

gga tat ata ggt gga gct aaa gtt ctt ggt aca gca cca ggt tcc gcg     480
```

-25-

```
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145             150             155             160

ggt ctg gtg cca cgc ggt agt act gca att ggt atg aaa gaa acc gct    528
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
            165             170             175

gct gct aaa ttc gaa cgc cag cac atg gac agc cca gat ctg ggt acc    576
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
            180             185             190

gat gac gac gac aag atg gga gtg aaa gtt ctt ttt gcc ctt att tgt    624
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
            195             200             205

att gct gtg gcc gag gcc aaa cca act gaa aac aat gaa gat ttc aac    672
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
    210             215             220

att gta gct gta gct agc aac ttt gct aca acg gat ctc gat gct gac    720
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225             230             235             240

cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt gag gta ctc aaa gaa    768
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
            245             250             255

atg gaa gcc aat gct agg aaa gct ggc tgc act agg gga tgt ctg ata    816
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
            260             265             270

tgc ctg tca cac atc aag tgt aca ccc aaa atg aag aag ttt atc cca    864
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
            275             280             285

gga aga tgc cac acc tat gaa gga gac aaa gaa agt gca cag gga gga    912
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
    290             295             300

ata gga gag gct att gtt gac att cct gaa att cct ggg ttt aag gat    960
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305             310             315             320

ttg gaa ccc atg gaa caa ttc att gca caa gtt gac cta tgt gta gac   1008
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
            325             330             335

tgc aca act gga tgc ctc aaa ggt ctt gcc aat gtg caa tgt tct gat   1056
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
            340             345             350

tta ctc aag aaa tgg ctg cca caa aga tgt gca act ttt gct agc aaa   1104
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
            355             360             365

att caa ggc caa gtg gac aaa ata aag ggt gcc ggt ggt gat           1146
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
            370             375             380
```

<210> 22
<211> 382
<212> PRT
<213> Gaussia

```
<400> 22
Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
1               5                   10                  15
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
            20                  25                  30
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
    35                  40                  45
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
50                  55                  60
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
65                  70                  75                  80
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
                85                  90                  95
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
            100                 105                 110
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
        115                 120                 125
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
    130                 135                 140
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145                 150                 155                 160
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
                165                 170                 175
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
            180                 185                 190
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
        195                 200                 205
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
    210                 215                 220
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225                 230                 235                 240
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
                245                 250                 255
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
            260                 265                 270
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
        275                 280                 285
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
    290                 295                 300
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305                 310                 315                 320
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
                325                 330                 335
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
            340                 345                 350
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
        355                 360                 365
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
    370                 375                 380


<210> 23
<211> 864
<212> DNA
<213> Renilla renifomis

<220>
<221> CDS
<222> (61)...(762)
<223> GFP Clone-1

<400> 23
ggcacgaggg tttcctgaca caataaaaac ctttcaaatt gtttctctgt agcagtaagt    60
atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc   108
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1               5                   10                  15
```

```
aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt      156
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
            20                  25                  30

ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta      204
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
            35                  40                  45

aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct      252
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
        50                  55                  60

ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc      300
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
 65                  70                  75                  80

gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac      348
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
                85                  90                  95

att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc      396
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
            100                 105                 110

ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat      444
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
            115                 120                 125

cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag      492
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
        130                 135                 140

cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa      540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145                 150                 155                 160

tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac      588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
                165                 170                 175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg      636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
            180                 185                 190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc      684
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
            195                 200                 205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca      732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
        210                 215                 220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc        782
Ile Lys Lys Ile Glu Gly Ser Leu Pro *
225                 230

tatgcacgta gcattttttt ggaaatataa gtggtattgt caataaaat attaaatata   842
aaaaaaaaaa aaaaaaaaaa aa                                            864
```

<220>
<221> CDS
<222> (57)...(758)
<223> GFP Clone-2

<400> 24
ggcacgaggc tgacacaata aaaaacctttt caaattgtttt ctctgtagca ggaagt atg   59
                                                                 Met
                                                                  1

gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc aac   107
Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile Asn
              5   10   15

tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt ggc   155
Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val Gly
          20   25   30

gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta aca   203
Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val Thr
      35   40   45

aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtt gct ttc   251
Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala Phe
  50   55   60   65

tca tat ggg aac aga gct tat act ggt tac·cca gaa gaa att tcc gac   299
Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser Asp
                  70   75   80

tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac att   347
Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn Ile
              85   90   95

cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc ttg   395
Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser Leu
          100   105   110

gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat cta   443
Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp Leu
      115   120   125

cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag cca   491
Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln Pro
130   135   140   145

tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa tgt   539
Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu Cys
                  150   155   160

ata ata gca ttc aaa ctt caa act ggc aaa cat ttc act tac cac atg   587
Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His Met
              165   170   175

agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg tat   635
Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu Tyr
          180   185   190

cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc agt   683
His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala Ser
          195   200   205

ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca atc   731
Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr Ile
210   215   220   225

-29-

```
aaa aaa att gaa ggc tct tta cca tag atatctatac acaattattc        778
Lys Lys Ile Glu Gly Ser Leu Pro  *
                            230

tatgcacgta gcattttttt ggaaatataa gtggtattgt tcaataaaat attaaatata   838
aaaaaaaaaa aaaaaaaaaa aa                                            860
```

```
<210> 25
<211> 873
<212> DNA
<213> Renilla reniformis

<220>
<221> CDS
<222> (61)...(762)
<223> GFP Clone-3

<400> 25
ggcacgaggg tttcctgaca caataaaaac ctttcaaatt gtttctctgt agcagtaagt   60
atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc   108
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1               5                  10                  15

aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt   156
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
            20                  25                  30

ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta   204
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
        35                  40                  45

aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct   252
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
    50                  55                  60

ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc   300
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65                  70                  75                  80

gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac   348
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
                85                  90                  95

att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc   396
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
            100                 105                 110

ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat   444
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
            115                 120                 125

cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag   492
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
    130                 135                 140

cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa   540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145                 150                 155                 160

tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac   588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
                165                 170                 175
```

```
atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg      636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
        180                 185                 190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc      684
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
        195                 200                 205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca      732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
    210                 215                 220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc        782
Ile Lys Lys Ile Glu Gly Ser Leu Pro *
225                 230

tatgcacgta gcattttttt ggaaatataa gtggtattgt tcaataaaat attaaatata    842
tgcttttgca aaaaaaaaaa aaaaaaaaa a                                    873
```

<210> 26
<211> 864
<212> DNA
<213> Renilla reniformis

<220>
<221> CDS
<222> (61)...(759)
<223> Human codon optimized Renilla reniformis GFP

<400> 26

```
ggcacgaggg tttcctgaca caataaaaac ctttcaaatt gtttctctgt agcagtaagt     60
atg gac ctg gcc aag ctg ggc ctg aag gag gtg atg ccc acc aag atc      108
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1               5                   10                  15

aac ctg gag ggc ctg gtg ggc gac cac gcc ttc tcg atg gag ggc gtg      156
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
            20                  25                  30

ggc gag ggc aac atc ttg gag ggc acc cag gag gtg aag atc agc gtg      204
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
        35                  40                  45

acc aag ggc gcc ccc ctg ccc ttc gcc ttc gac atc gtg agc gtg gcc      252
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
    50                  55                  60

ttc agc tac ggc aac cgg gcc tac acc ggc tac ccc gag gag atc agc      300
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65                  70                  75                  80

gac tac ttc ctg cag agc ttc ccc gag ggc ttc acc tac gag cgg aac      348
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
                85                  90                  95

atc cgg tac cag gac ggc ggc acc gcc atc gtg aag agc gac atc agc      396
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
        100                 105                 110

ctg gag gac ggc aag ttc atc gtg aac gtg gac ttc aag gcc aag gac      444
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
        115                 120                 125

ctg cgg cgg atg ggc ccc gtg atg cag cag gac atc gtg ggc atg cag      492
```

```
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
    130             135             140

ccc agc tac gag agc atg tac acc aac gtg acc agc gtg atc ggc gag    540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145             150             155             160

tgc atc atc gcc ttc aag ctg cag acc ggc aag cac ttc acc tac cac    588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
                165             170             175

atg cgg acc gtg tac aag agc aag aag ccc gtg gag acc atg ccc ctg    636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
            180             185             190

tac cac ttc atc cag cac cgg ctg gtg aag acc aac gtg gac acc gcc    684
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
            195             200             205

agc ggc tac gtg gtg cag cac gag aca gcc atc gcc gcc cac agc acc    732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
    210             215             220

atc aag aag atc gag ggc agc ctg ccc tagatacctg tacacaatta          779
Ile Lys Lys Ile Glu Gly Ser Leu Pro
225             230

ttctatgcac gtagcatttt tttggaaata taagtggtat tgttcaataa aatattaaat    839
ataaaaaaaa aaaaaaaaaa aaaaa                                          864
```

<210> 27
<211> 233
<212> PRT
<213> Renilla reniformis

<400> 27
```
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1               5                   10                  15
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
            20                  25                  30
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
        35                  40                  45
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
    50                  55                  60
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65                  70                  75                  80
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
                85                  90                  95
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
            100                 105                 110
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
            115                 120                 125
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
            130                 135                 140
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145                 150                 155                 160
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
                165                 170                 175
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
            180                 185                 190
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
            195                 200                 205
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
    210                 215                 220
Ile Lys Lys Ile Glu Gly Ser Leu Pro
```

-32-

225   230

<210> 28
<211> 861
<212> DNA
<213> Pleuromamma

<220>
<221> CDS
<222> (148)...(741)
<223> Pleuormamma luciferase

<400> 28
cggcacgaga ttttgtctgt ggtgattggg attgtctgtc tctcaggtca agcagaaagt   60
tcgctgaaag gtgatttctg tagtgatgtt tccttctggg atgtgatcaa gtacaacact   120
gagagtcgac aatgctgtga cacaaaa atg ctt aga aat tgc gct agg aag caa   174
                                Met Leu Arg Asn Cys Ala Arg Lys Gln
                                  1   5

gag caa gtt tgc gcc gat gtg acc gag atg aaa tgc caa gca gtt gct   222
Glu Gln Val Cys Ala Asp Val Thr Glu Met Lys Cys Gln Ala Val Ala
 10   15   20   25

tgg gcc gac tgt gga ccc aga ttt gat tcc act ggc agg aat aga tgc   270
Trp Ala Asp Cys Gly Pro Arg Phe Asp Ser Thr Gly Arg Asn Arg Cys
                30   35   40

caa gtt caa tac aag gac tac gcg tac aag tcc tgc gtg gaa gtt gat   318
Gln Val Gln Tyr Lys Asp Tyr Ala Tyr Lys Ser Cys Val Glu Val Asp
                45   50   55

tac act gta ccg cac agg aag caa gtt cca gag tgc aaa caa gtc act   366
Tyr Thr Val Pro His Arg Lys Gln Val Pro Glu Cys Lys Gln Val Thr
                60   65   70

aaa gat aac tgc gtt act gat tgg gaa gtt gac gcc aat ggc aac aag   414
Lys Asp Asn Cys Val Thr Asp Trp Glu Val Asp Ala Asn Gly Asn Lys
         75   80   85

gtt tgg ggt ggt acc gag aaa tgc act cct gtc act tgg gaa gaa tgt   462
Val Trp Gly Gly Thr Glu Lys Cys Thr Pro Val Thr Trp Glu Glu Cys
 90   95   100   105

aat atc gtg gag aaa gat gta gat ttt cca act gtc aag acg gaa tgc   510
Asn Ile Val Glu Lys Asp Val Asp Phe Pro Thr Val Lys Thr Glu Cys
                110   115   120

ggc atc ctg tct cac ctt aag tat gca gac ttc ata gag gga cct tcc   558
Gly Ile Leu Ser His Leu Lys Tyr Ala Asp Phe Ile Glu Gly Pro Ser
                125   130   135

cac tct ttg tct atg aga acc aat tgt cag gtc aag agt tca ttg gac   606
His Ser Leu Ser Met Arg Thr Asn Cys Gln Val Lys Ser Ser Leu Asp
                140   145   150

tgc cgg cct gtt aag acc agg aag tgt gca acg gtc gag tac cac gaa   654
Cys Arg Pro Val Lys Thr Arg Lys Cys Ala Thr Val Glu Tyr His Glu
                155   160   165

tgc agc atg aag ccc caa gaa gac tgc agc cca gtc act gtt cat att   702
Cys Ser Met Lys Pro Gln Glu Asp Cys Ser Pro Val Thr Val His Ile
170   175   180   185

cct gac cag gag aaa gtt cac cag aag aag tgc ctc aca taaatgttat   751
Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr

-33-

```
Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr
            190                 195
```

```
caattttagc tcttactaat ttaaacataa taaatatcac atcgaagccc tttattttat      811
agaagtgtaa tgcttgaata aatctagtga ataaaaaaaa aaaaaaaaaa                  861
```

```
<210> 29
<211> 198
<212> PRT
<213> Pleuromamma
```

```
<400> 29
Met Leu Arg Asn Cys Ala Arg Lys Gln Glu Gln Val Cys Ala Asp Val
 1               5                  10                  15
Thr Glu Met Lys Cys Gln Ala Val Ala Trp Ala Asp Cys Gly Pro Arg
            20                  25                  30
Phe Asp Ser Thr Gly Arg Asn Arg Cys Gln Val Gln Tyr Lys Asp Tyr
        35                  40                  45
Ala Tyr Lys Ser Cys Val Glu Val Asp Tyr Thr Val Pro His Arg Lys
    50                  55                  60
Gln Val Pro Glu Cys Lys Gln Val Thr Lys Asp Asn Cys Val Thr Asp
65                  70                  75                  80
Trp Glu Val Asp Ala Asn Gly Asn Lys Val Trp Gly Gly Thr Glu Lys
                85                  90                  95
Cys Thr Pro Val Thr Trp Glu Glu Cys Asn Ile Val Glu Lys Asp Val
            100                 105                 110
Asp Phe Pro Thr Val Lys Thr Glu Cys Gly Ile Leu Ser His Leu Lys
        115                 120                 125
Tyr Ala Asp Phe Ile Glu Gly Pro Ser His Ser Leu Ser Met Arg Thr
    130                 135                 140
Asn Cys Gln Val Lys Ser Ser Leu Asp Cys Arg Pro Val Lys Thr Arg
145                 150                 155                 160
Lys Cys Ala Thr Val Glu Tyr His Glu Cys Ser Met Lys Pro Gln Glu
                165                 170                 175
Asp Cys Ser Pro Val Thr Val His Ile Pro Asp Gln Glu Lys Val His
            180                 185                 190
Gln Lys Lys Cys Leu Thr
        195
```

```
<210> 30
<211> 1104
<212> DNA
<213> Ptilosarcus gurneyi
```

```
<220>
<221> CDS
<222> (34)...(747)
<223> Ptilosarcus Green Flourescent Protein
```

```
<400> 30
tcggcacgag ctggcctcca cactttagac aaa atg aac cgc aac gta tta aag      54
                                    Met Asn Arg Asn Val Leu Lys
                                     1               5
```

```
aac act gga ctg aaa gag att atg tcg gca aaa gct agc gtt gaa gga      102
Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly
            10                  15                  20
```

```
atc gtg aac aat cac gtt ttt tcc atg gaa gga ttt gga aaa ggc aat      150
Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn
    25                  30                  35
```

```
gta tta ttt gga aac caa ttg atg caa atc cgg gtt aca aag gga ggt      198
Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly
    40                  45                  50                  55
```

```
ccg ttg cca ttc gct ttc gat att gtt tcc ata gct ttc caa tac ggg    246
Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly
            60              65                      70

aat cgc act ttc acg aaa tac cca gac gac att gcg gac tac ttt gtt    294
Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val
        75                  80                  85

caa tca ttc ccg gct gga ttt ttc tac gaa aga aat cta cgc ttt gaa    342
Gln Ser Phe Pro Ala Gly Phe Phe Tyr Glu Arg Asn Leu Arg Phe Glu
        90                  95                  100

gat ggc gcc att gtt gac att cgt tca gat ata agt tta gaa gat gat    390
Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp
    105                 110                 115

aag ttc cac tac aaa gtg gag tat aga ggc aac ggt ttc cct agt aac    438
Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn
120             125             130                 135

gga ccc gtg atg caa aaa gcc atc ctc ggc atg gag cca tcg ttt gag    486
Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu
            140                 145                 150

gtg gtc tac atg aac agc ggc gtt ctg gtg ggc gaa gta gat ctc gtt    534
Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val
            155                 160                 165

tac aaa ctc gag tca ggg aac tat tac tcg tgc cac atg aaa acg ttt    582
Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe
        170                 175                 180

tac aga tcc aaa ggt gga gtg aaa gaa ttc ccg gaa tat cac ttt atc    630
Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile
    185                 190                 195

cat cat cgt ctg gag aaa acc tac gtg gaa gaa gga agc ttc gtg gaa    678
His His Arg Leu Glu Lys Thr Tyr Val Glu Glu Gly Ser Phe Val Glu
200             205                 210                 215

caa cac gag acg gcc att gca caa ctg acc aca att gga aaa cct ctg    726
Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu
                220                 225                 230

ggc tcc ctt cat gaa tgg gtg tagaaaatga ccaatatact ggggaaaccg    777
Gly Ser Leu His Glu Trp Val
                235

ataaccgttt ggaagcttgt gtatacaaat tatttggggt cattttgtaa tgtgtatgtg    837
tgttgtatga tcaatagacg tcgtcattca tagcttgaat ccttcagcaa aagaaacctc    897
gaagcatatt gaaacctcga agcatattga aacctcgacg gagagcgtaa agagaccgca    957
caaattaacg cgtttcaacc agcagttgga atctttaaac cgatcaaaac tattaatata    1017
aatatatata ccctgtataa cttatatata tctatatagt ttgatattga ttaaatctgt    1077
tcttgatcaa aaaaaaaaa aaaaaaa    1104


<210> 31
<211> 1279
<212> DNA
<213> Ptilosarcus gurneyi
```

<223> Ptilosarcus Green Flourescent Protein (GFP)

<400> 31

```
gacaaa atg aac cgc aac gta tta aag aac act gga ctg aaa gag att        48
       Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile
        1               5                  10

atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt        96
Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe
 15              20                  25                  30

tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg       144
Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu
                 35                  40                  45

atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac       192
Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp
             50                  55                  60

att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac       240
Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr
             65                  70                  75

cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt       288
Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe
         80                  85                  90

ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att       336
Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile
 95                  100                 105                 110

cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag       384
Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu
                 115                 120                 125

tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc       432
Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala
             130                 135                 140

atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc       480
Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly
         145                 150                 155

gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac       528
Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn
     160                 165                 170

tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg       576
Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val
175                 180                 185                 190

aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc       624
Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr
                 195                 200                 205

tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca       672
Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala
             210                 215                 220

caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg       720
Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
             225                 230                 235

tagaaaatga ccaatatact ggggaaaatc accaatatac tggggaaaat gaccaattta    780
ctggggaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat    840
```

-36-

```
ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca      900
aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt      960
gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga     1020
cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc     1080
gacggagagc ataaagagac cgcacgtaca caattataa taccagcagt tggaatcttt      1140
aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata     1200
tctacatagt ttgatattga ttaaatctgt tcttgatcac taaaaaaaaa aaaaaaaaaa     1260
aaaaaaaaaa aaaaaaaaa                                                  1279
```

<210> 32
<211> 238
<212> PRT
<213> Ptilosarcus gurneyi

<400> 32

```
Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
 1               5                  10                  15
Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
            20                  25                  30
Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
        35                  40                  45
Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
    50                  55                  60
Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65                  70                  75                  80
Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
                85                  90                  95
Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
            100                 105                 110
Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
            115                 120                 125
Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
            130                 135                 140
Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145                 150                 155                 160
Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
                165                 170                 175
Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
                180                 185                 190
Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
            195                 200                 205
Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
            210                 215                 220
Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225                 230                 235
```

<210> 33
<211> 233
<212> PRT
<213> Renilla Reniformis mutein

<400> 33

```
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1               5                  10                  15
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
            20                  25                  30
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
        35                  40                  45
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
    50                  55                  60
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65                  70                  75                  80
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
                85                  90                  95
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Asp Ser Asp Ile Ser
```

-37-

```
                 100                      105                      110
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Asp Asp
         115                      120                  125
Leu Arg Asp Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
         130                      135                  140
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145                      150                      155                  160
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys Asp Phe Thr Tyr His
                 165                      170                      175
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
             180                      185                      190
Tyr His Phe Ile Gln His Asp Leu Val Lys Thr Asn Val Asp Thr Ala
         195                      200                      205
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
210                      215                      220
Ile Asp Lys Ile Glu Gly Ser Leu Pro
225                      230
```